

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/831,804
Source: IFW16
Date Processed by STIC: 4/19/05

ENTERED

**Edit authorized by Examiner*

**CRF Errors Edited by the STIC Systems
Branch**

Serial Number: 09/831,804

CRF Edit Date: 4/19/05
Edited by: AK

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

✓
___ Other:
corrected <1207 response - translated to English



IFW16

RAW SEQUENCE LISTING

DATE: 04/19/2005

PATENT APPLICATION: US/09/831,804

TIME: 16:35:27

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\04192005\I831804.raw

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3 <110> APPLICANT: Hoechst Marion Roussel
4   Bordon-Pallier, F.
5   Camier, S.
6   Sentenac, A.
8 <120> TITLE OF INVENTION: GSne tfIIIA of Candida albicans (CATfIIIA) and the
9   protein coded CATfIIIA
11 <130> FILE REFERENCE: 146.1365
13 <140> CURRENT APPLICATION NUMBER: US 09/831,804
C--> 14 <141> CURRENT FILING DATE: 2001-07-23
16 <160> NUMBER OF SEQ ID NOS: 9
18 <170> SOFTWARE: PatentIn Vers. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2060
22 <212> TYPE: DNA
23 <213> ORGANISM: Candida albicans
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28 tagtaaatat ccaatcattg ggcttcagtg tgaatggggg ttgtcaatct cttggtgtag 120
30 aaataggcgc aggcctccga atcccaaaaa aagaagaatc aggatgtctc ggctgcaaga 180
32 tttgtagcca tggcaaatgc cgaaaaatga aaaaaaaaaa aaagtctact gggcccacct 240
34 acaaaaaggaa aagtgattga actagatcag tagtggctcg gaccctctat aattttataa 300
36 tattgtcacg ggcttttagaa tttgtataat tgtgtgtctg acactctgtg gttaatatct 360
38 ggacatctcg ttccccttgt gaagggtcgt ctgtaatgaa ttcgatgaca agaataatat 420
40 gactttgtct acttcataga gtgccgactt gattattatt gagctttatc ctctgtaata 480
42 tatcgtaacc acttgactta ttcccttgtt gtgggattca ctttggatga tgatgttaac 540
44 caaatgtaat tggtaacaatc ctttttgtcc ttgtcgcgac ttcccttaat atcgcgactt 600
46 atttcattaa tgagacgcaa cgcattcctc tctccataga aaaaaaaaaa aacaaactga 660
48 aaaaataaac agcggacctc atctcttttt ttcaaataca ctttttatta ctttattcaa 720
50 tgagtgaag tgacgaaacc aaatcgatat catctttaat atcttcttct tcttcatcac 780
52 gtcccaaaaa gtatatattgc acatatgaag ggtgtgataa agcctataat cgaccatcat 840
54 tattagagca acatttaaga acccacagta atgatcgacc gtataaatgt acagtggacg 900
56 attgtgataa agcatttttc agaaaatcac atttggaac acatattgta tcacattccg 960
58 aaaaaaaacc attccattgt tcagtgtgtg gtaaagggtt taattctcga caacacttga 1020
60 aaagacatga aatcacccat acaaagtcac ttaaattgtac atttgaaaat tgtcaagaag 1080
62 cttttataaa acatcaatct ttaagacatc atatattatc tgttcatgaa aaaacattaa 1140
64 cgtgtaaaca atgtaataaa gttttcactc gaccttcaaa attagcacia cataaattaa 1200
66 aacatcatgg tggatctcct gcttatcaat gtgatcatcc tgggtgtttt aaaaatttcc 1260
68 aaacttggtc agtattacaa tttcatataa aacaactgca tccaaaactt aaatgtccta 1320
70 aatgtggtaa aggttgtgtt gggaaaaaag gtttatcttc acatatgtta agtcatgatg 1380
72 attctacat gatcaaaata tggacttgtg attattgtga tgtggggaaa tttgcaaaga 1440
74 aaaatgaatt agttgaacat tataatatct tccatgatgg taatatccct gatgatttat 1500
76 taaaggaaac tgaagtgaac aaattagaga acctattaga tcaaggatcg aaattaaata 1560
78 atttgcataa attagaaaca gagaaattaa aagtggaaga agatgaagaa gatgaagaag 1620

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82 taaaatcatt tactgcttct ttggaagggtt caaagagtgt ttctaaactt attctgaata 1740
84 gtgggaagaa gatcaattgt cctaagaata attgtgatag aatgttttct agagaatatg 1800
86 atttacgtcg acatttgaaa tggcatgatg ataatttaca aagaattgag tcattcttaa 1860
88 atagtataga aaaagaagaa actccagaag gtgaaccatt ggtaaaaaaa gccaggatgg 1920
90 atttattgcc aaatgaaaca tcagtgattt ctcgataata tacattttaa attatattaa 1980
92 cattttttatt tcctttaatt tttatttttt gtgggctttt tattttacat tattttaactt 2040
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98 <211> LENGTH: 1239
99 <212> TYPE: DNA
100 <213> ORGANISM: Candida albicans
102 <220> FEATURE:
103 <221> NAME/KEY: CDS
104 <222> LOCATION: (1)..(1236)
106 <400> SEQUENCE: 2
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108 Met Ser Glu Ser Asp Glu Thr Lys Ser Ile Ser Ser Leu Ile Ser Ser
109 1 5 10 15
111 tct tct tca tca cgt ccc aaa aag tat att tgc aca tat gaa ggg tgt 96
112 Ser Ser Ser Ser Arg Pro Lys Lys Tyr Ile Cys Thr Tyr Glu Gly Cys
113 20 25 30
115 gat aaa gcc tat aat cga cca tca tta tta gag caa cat tta aga acc 144
116 Asp Lys Ala Tyr Asn Arg Pro Ser Leu Leu Glu Gln His Leu Arg Thr
117 35 40 45
119 cac agt aat gat cga ccg tat aaa tgt aca gtg gac gat tgt gat aaa 192
120 His Ser Asn Asp Arg Pro Tyr Lys Cys Thr Val Asp Asp Cys Asp Lys
121 50 55 60
123 gca ttt ttc aga aaa tca cat ttg gaa aca cat att gta tca cat tcc 240
124 Ala Phe Phe Arg Lys Ser His Leu Glu Thr His Ile Val Ser His Ser
125 65 70 75 80
127 gaa aaa aaa cca ttc cat tgt tca gtg tgt ggt aaa ggg gtt aat tct 288
128 Glu Lys Lys Pro Phe His Cys Ser Val Cys Gly Lys Gly Val Asn Ser
129 85 90 95
131 cga caa cac ttg aaa aga cat gaa atc acc cat aca aag tca ttt aaa 336
132 Arg Gln His Leu Lys Arg His Glu Ile Thr His Thr Lys Ser Phe Lys
133 100 105 110
135 tgt aca ttt gaa aat tgt caa gaa gca ttt tat aaa cat caa tct tta 384
136 Cys Thr Phe Glu Asn Cys Gln Glu Ala Phe Tyr Lys His Gln Ser Leu
137 115 120 125
139 aga cat cat ata tta tct gtt cat gaa aaa aca tta acg tgt aaa caa 432
140 Arg His His Ile Leu Ser Val His Glu Lys Thr Leu Thr Cys Lys Gln
141 130 135 140
143 tgt aat aaa gtt ttc act cga cct tca aaa tta gca caa cat aaa tta 480
144 Cys Asn Lys Val Phe Thr Arg Pro Ser Lys Leu Ala Gln His Lys Leu
145 145 150 155 160
147 aaa cat cat ggt gga tct cct gct tat caa tgt gat cat cct ggt tgt 528
148 Lys His His Gly Gly Ser Pro Ala Tyr Gln Cys Asp His Pro Gly Cys
149 165 170 175

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151 ttt aaa aat ttc caa act tgg tca gta tta caa ttt cat ata aaa caa 576
152 Phe Lys Asn Phe Gln Thr Trp Ser Val Leu Gln Phe His Ile Lys Gln
153 180 185 190
155 ctg cat cca aaa ctt aaa tgt cct aaa tgt ggt aaa ggt tgt gtt ggg 624
156 Ser His Pro Lys Leu Lys Cys Pro Lys Cys Gly Lys Gly Cys Val Gly
157 195 200 205
159 aaa aaa ggt tta tct tca cat atg tta agt cat gat gat tct acc atg 672
160 Lys Lys Gly Leu Ser Ser His Met Leu Ser His Asp Asp Ser Thr Met
161 210 215 220
163 atc aaa ata tgg act tgt gat tat tgt gat gtg ggg aaa ttt gca aag 720
164 Ile Lys Ile Trp Thr Cys Asp Tyr Cys Asp Val Gly Lys Phe Ala Lys
165 225 230 235 240
167 aaa aat gaa tta gtt gaa cat tat aat atc ttc cat gat ggt aat atc 768
168 Lys Asn Glu Leu Val Glu His Tyr Asn Ile Phe His Asp Gly Asn Ile
169 245 250 255
171 cct gat gat tta tta aag gaa act gaa gtg aaa aaa tta gag aac cta 816
172 Pro Asp Asp Leu Leu Lys Glu Thr Glu Val Lys Lys Leu Glu Asn Leu
173 260 265 270
175 tta gat caa gga tcg aaa tta aat aat ttg cat gaa tta gaa aca gag 864
176 Leu Asp Gln Gly Ser Lys Leu Asn Asn Leu His Glu Leu Glu Thr Glu
177 275 280 285
179 aaa tta aaa gtg gaa gaa gat gaa gaa gat gaa gaa gat agt cta gat 912
180 Lys Leu Lys Val Glu Glu Asp Glu Glu Asp Glu Glu Asp Ser Leu Asp
181 290 295 300
183 gaa aaa aga agt gat gtt aga tca gac tca atg tca gct caa aga tca 960
184 Glu Lys Arg Ser Asp Val Arg Ser Asp Ser Met Ser Ala Gln Arg Ser
185 305 310 315 320
187 ata aaa tca ttt act gct tct ttg gaa ggt tca aag agt gtt tct aaa 1008
188 Ile Lys Ser Phe Thr Ala Ser Leu Glu Gly Ser Lys Ser Val Ser Lys
189 325 330 335
191 ctt att ctg aat agt ggg aag aag atc aat tgt cct aag aat aat tgt 1056
192 Leu Ile Ser Asn Ser Gly Lys Lys Ile Asn Cys Pro Lys Asn Asn Cys
193 340 345 350
195 gat aga atg ttt tct aga gaa tat gat tta cgt cga cat ttg aaa tgg 1104
196 Asp Arg Met Phe Ser Arg Glu Tyr Asp Leu Arg Arg His Leu Lys Trp
197 355 360 365
199 cat gat gat aat tta caa aga att gag tca ttc tta aat agt ata gaa 1152
200 His Asp Asp Asn Leu Gln Arg Ile Glu Ser Phe Leu Asn Ser Ile Glu
201 370 375 380
203 aaa gaa gaa act cca gaa ggt gaa cca ttg gtt aaa aaa gcc agg atg 1200
204 Lys Glu Glu Thr Pro Glu Gly Glu Pro Leu Val Lys Lys Ala Arg Met
205 385 390 395 400
207 gat tta ttg cca aat gaa aca tca gtg att tct cga taa 1239
208 Asp Leu Leu Pro Asn Glu Thr Ser Val Ile Ser Arg
209 405 410
212 <210> SEQ ID NO: 3
213 <211> LENGTH: 412
214 <212> TYPE: PRT
215 <213> ORGANISM: Candida albicans

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217 <400> SEQUENCE: 3

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218 Met Ser Glu Ser Asp Glu Thr Lys Ser Ile Ser Ser Leu Ile Ser Ser
219   1           5           10           15
221 Ser Ser Ser Ser Arg Pro Lys Lys Tyr Ile Cys Thr Tyr Glu Gly Cys
222           20           25           30
224 Asp Lys Ala Tyr Asn Arg Pro Ser Leu Leu Glu Gln His Leu Arg Thr
225           35           40           45
227 His Ser Asn Asp Arg Pro Tyr Lys Cys Thr Val Asp Asp Cys Asp Lys
228   50           55           60
230 Ala Phe Phe Arg Lys Ser His Leu Glu Thr His Ile Val Ser His Ser
231  65           70           75           80
233 Glu Lys Lys Pro Phe His Cys Ser Val Cys Gly Lys Gly Val Asn Ser
234           85           90           95
236 Arg Gln His Leu Lys Arg His Glu Ile Thr His Thr Lys Ser Phe Lys
237           100          105          110
239 Cys Thr Phe Glu Asn Cys Gln Glu Ala Phe Tyr Lys His Gln Ser Leu
240          115          120          125
242 Arg His His Ile Leu Ser Val His Glu Lys Thr Leu Thr Cys Lys Gln
243          130          135          140
245 Cys Asn Lys Val Phe Thr Arg Pro Ser Lys Leu Ala Gln His Lys Leu
246 145          150          155          160
248 Lys His His Gly Gly Ser Pro Ala Tyr Gln Cys Asp His Pro Gly Cys
249           165          170          175
251 Phe Lys Asn Phe Gln Thr Trp Ser Val Leu Gln Phe His Ile Lys Gln
252           180          185          190
254 Ser His Pro Lys Leu Lys Cys Pro Lys Cys Gly Lys Gly Cys Val Gly
255           195          200          205
257 Lys Lys Gly Leu Ser Ser His Met Leu Ser His Asp Asp Ser Thr Met
258          210          215          220
260 Ile Lys Ile Trp Thr Cys Asp Tyr Cys Asp Val Gly Lys Phe Ala Lys
261 225          230          235          240
263 Lys Asn Glu Leu Val Glu His Tyr Asn Ile Phe His Asp Gly Asn Ile
264           245          250          255
266 Pro Asp Asp Leu Leu Lys Glu Thr Glu Val Lys Lys Leu Glu Asn Leu
267           260          265          270
269 Leu Asp Gln Gly Ser Lys Leu Asn Asn Leu His Glu Leu Glu Thr Glu
270           275          280          285
272 Lys Leu Lys Val Glu Glu Asp Glu Glu Asp Glu Glu Asp Ser Leu Asp
273          290          295          300
275 Glu Lys Arg Ser Asp Val Arg Ser Asp Ser Met Ser Ala Gln Arg Ser
276 305          310          315          320
278 Ile Lys Ser Phe Thr Ala Ser Leu Glu Gly Ser Lys Ser Val Ser Lys
279           325          330          335
281 Leu Ile Ser Asn Ser Gly Lys Lys Ile Asn Cys Pro Lys Asn Asn Cys
282           340          345          350
284 Asp Arg Met Phe Ser Arg Glu Tyr Asp Leu Arg Arg His Leu Lys Trp
285           355          360          365
287 His Asp Asp Asn Leu Gln Arg Ile Glu Ser Phe Leu Asn Ser Ile Glu
288          370          375          380

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290 Lys Glu Glu Thr Pro Glu Gly Glu Pro Leu Val Lys Lys Ala Arg Met
291 385                               390                               395                               400
293 Asp Leu Leu Pro Asn Glu Thr Ser Val Ile Ser Arg
294                               405                               410
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298 <211> LENGTH: 21
299 <212> TYPE: DNA
300 <213> ORGANISM: Candida albicans
302 <400> SEQUENCE: 4
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307 <211> LENGTH: 24
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309 <213> ORGANISM: Candida albicans
311 <400> SEQUENCE: 5
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316 <211> LENGTH: 23
317 <212> TYPE: DNA
318 <213> ORGANISM: Candida albicans
320 <400> SEQUENCE: 6
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325 <211> LENGTH: 25
326 <212> TYPE: DNA
327 <213> ORGANISM: Candida albicans
329 <400> SEQUENCE: 7
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334 <211> LENGTH: 27
335 <212> TYPE: DNA
336 <213> ORGANISM: Candida albicans
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343 <211> LENGTH: 27
344 <212> TYPE: DNA
345 <213> ORGANISM: Candida albicans
347 <400> SEQUENCE: 9
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/831,804

DATE: 04/19/2005

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Input Set : A:\PTO.AMC.txt

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date



PCT

RAW SEQUENCE LISTING

DATE: 04/19/2005

PATENT APPLICATION: US/09/831,804

TIME: 16:31:51

Input Set : N:\AMC\US09831804.raw

Output Set: N:\CRF4\04192005\I831804.raw

1 <110> APPLICANT: Hoechst Marion Roussel
 2 Bordon-Pallier, F.
 3 Camier, S.
 4 Sentenac, A.

5 <120> TITLE OF INVENTION: GSne tfIIIA de Candida albicans (CATfIIIA) et la
 6 prot,ine cod,e CATfIIIA.

7 <130> FILE REFERENCE: 146.1365

8 <140> CURRENT APPLICATION NUMBER: US/09/831,804

9 <141> CURRENT FILING DATE: 2001-07-23

10 <160> NUMBER OF SEQ ID NOS: 9

11 <170> SOFTWARE: PatentIn Vers. 2.0

13 <210> SEQ ID NO: 1

14 <211> LENGTH: 2060

15 <212> TYPE: DNA

16 <213> ORGANISM: Candida albicans

17 <400> SEQUENCE: 1

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20	aaatagggcg	aggcctccga	atcccaaaaa	aagaagaatc	aggatgtctc	ggctgcaaga	180
21	tttgtagcca	tggcaaagtc	cgaaaaatga	aaaaaaaaaa	aaagtctact	gggcccacct	240
22	acaaaaggaa	aagtgattga	actagatcag	tagtgggtctg	gacctcttat	aattttataa	300
23	tattgtcacg	ggcttttaga	tttgtataat	tgtgtgtctg	acactctgtg	gttaatatct	360
24	ggacatctcg	ttccccttgt	gaagggtcgt	ctgtaatgaa	ttcatgatca	agaataatat	420
25	gactttgtct	acttcataga	gtgccgactt	gattattatt	gagctttatc	ctctgtaata	480
26	tatcgtaacc	acttgactta	tttccttgtt	gtgggattca	ctttggatga	tgatgttaac	540
27	caaatgtaat	tggtacaatc	ctttttgtcc	ttgtcgcgac	ttcctttaat	atcgcgactt	600
28	atttcattaa	tgagacgcaa	cgcattcctc	tctccataga	aaaaaaaaat	aacaaactga	660
29	aaaaataaac	agcggacctc	atctcttttt	ttcaaattcca	ctttttatta	ctttattcaa	720
30	tgagtgaag	tgacgaaacc	aaatcgatat	catctttaat	atcttcttct	tcttcatcac	780
31	gtcccaaaaa	gtatatttgc	acatatgaag	ggtgtgataa	agcctataat	cgaccatcat	840
32	tattagagca	acatttaaga	accacagta	atgatcgacc	gtataaatgt	acagtggacg	900
33	attgtgataa	agcatttttc	agaaaatcac	atttggaaac	acatatgtta	tcacattccg	960
34	aaaaaaaaacc	attccattgt	tcaagtgtgt	gtaaaggggt	taattctcga	caacacttga	1020
35	aaagacatga	aatcacccat	acaaagtcac	ttaaattgtac	atttgaaaat	tgtcaagaag	1080
36	cattttataa	acatcaatct	ttaagacatc	atatattatc	tgttcatgaa	aaaacattaa	1140
37	cgtgtaaaca	atgtaataaa	gttttcactc	gaccttcaaa	attagcacia	cataaattaa	1200
38	aacatcatgg	tggatctcct	gcttatcaat	gtgatcatcc	tgggtgtttt	aaaaatttcc	1260
39	aaacttggtc	agtattacaa	tttcatataa	aacaactgca	tccaaaactt	aatgtccta	1320
40	aatgtggtaa	aggttgtgtt	gggaaaaaag	gtttatcttc	acatatgtta	agtcatgatg	1380
41	attctaccat	gatcaaaata	tggacttggt	attattgtga	tgtggggaaa	tttgcaaga	1440
42	aaaatgaatt	agttgaacat	tataatatct	tccatgatgg	taatattccct	gatgatttat	1500
43	taaaggaaac	tgaagtgaac	aaattagaga	acctattaga	tcaaggatcg	aaattaaata	1560
44	atttgcacga	attagaacaa	gagaaattaa	aagtggaaga	agatgaagaa	gatgaagaag	1620

use English in a U.S. application

**Does Not Comply
Corrected Diskette Needed**

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46   taaaatcatt tactgcttct ttggaagggtt caaagagtgt ttctaaactt attctgaata 1740
47   gtgggaagaa gatcaattgt cctaagaata attgtgatag aatgttttct agagaatatg 1800
48   atttacgtcg acatttgaaa tggcatgatg ataatttaca aagaattgag tcattcttaa 1860
49   atagtataga aaaagaagaa actccagaag gtgaaccatt ggtaaaaaaa gccaggatgg 1920
50   atttattgcc aaatgaaaca tcagtgatgt ctcgataata tacattttaa attatattaa 1980
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54 <210> SEQ ID NO: 2
55 <211> LENGTH: 1239
56 <212> TYPE: DNA
57 <213> ORGANISM: Candida albicans
58 <220> FEATURE:
59 <221> NAME/KEY: CDS
60 <222> LOCATION: (1)..(1236)
61 <400> SEQUENCE: 2'
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64   1 5 10 15
65   tct tct tca tca cgt ccc aaa aag tat att tgc aca tat gaa ggg tgt 96
66   Ser Ser Ser Ser Arg Pro Lys Lys Tyr Ile Cys Thr Tyr Glu Gly Cys
67   20 25 30
68   gat aaa gcc tat aat cga cca tca tta tta gag caa cat tta aga acc 144
69   Asp Lys Ala Tyr Asn Arg Pro Ser Leu Leu Glu Gln His Leu Arg Thr
70   35 40 45
71   cac agt aat gat cga ccg tat aaa tgt aca gtg gac gat tgt gat aaa 192
72   His Ser Asn Asp Arg Pro Tyr Lys Cys Thr Val Asp Asp Cys Asp Lys
73   50 55 60
74   gca ttt ttc aga aaa tca cat ttg gaa aca cat att gta tca cat tcc 240
75   Ala Phe Phe Arg Lys Ser His Leu Glu Thr His Ile Val Ser His Ser
76   65 70 75 80
77   gaa aaa aaa cca ttc cat tgt tca gtg tgt ggt aaa ggg gtt aat tct 288
78   Glu Lys Lys Pro Phe His Cys Ser Val Cys Gly Lys Gly Val Asn Ser
79   85 90 95
80   cga caa cac ttg aaa aga cat gaa atc acc cat aca aag tca ttt aaa 336
81   Arg Gln His Leu Lys Arg His Glu Ile Thr His Thr Lys Ser Phe Lys
82   100 105 110
83   tgt aca ttt gaa aat tgt caa gaa gca ttt tat aaa cat caa tct tta 384
84   Cys Thr Phe Glu Asn Cys Gln Glu Ala Phe Tyr Lys His Gln Ser Leu
85   115 120 125
86   aga cat cat ata tta tct gtt cat gaa aaa aca tta acg tgt aaa caa 432
87   Arg His His Ile Leu Ser Val His Glu Lys Thr Leu Thr Cys Lys Gln
88   130 135 140
89   tgt aat aaa gtt ttc act cga cct tca aaa tta gca caa cat aaa tta 480
90   Cys Asn Lys Val Phe Thr Arg Pro Ser Lys Leu Ala Gln His Lys Leu
91   145 150 155 160
92   aaa cat cat ggt gga tct cct gct tat caa tgt gat cat cct ggt tgt 528
93   Lys His His Gly Gly Ser Pro Ala Tyr Gln Cys Asp His Pro Gly Cys
94   165 170 175

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95   ttt aaa aat ttc caa act tgg tca gta tta caa ttt cat ata aaa caa   576
96   Phe Lys Asn Phe Gln Thr Trp Ser Val Leu Gln Phe His Ile Lys Gln
97           180                               185                               190
98   ctg cat cca aaa ctt aaa tgt cct aaa tgt ggt aaa ggt tgt gtt ggg   624
99   Ser His Pro Lys Leu Lys Cys Pro Lys Cys Gly Lys Gly Cys Val Gly
100          195                               200                               205
101   aaa aaa ggt tta tct tca cat atg tta agt cat gat gat tct acc atg   672
102   Lys Lys Gly Leu Ser Ser His Met Leu Ser His Asp Asp Ser Thr Met
103          210                               215                               220
104   atc aaa ata tgg act tgt gat tat tgt gat gtg ggg aaa ttt gca aag   720
105   Ile Lys Ile Trp Thr Cys Asp Tyr Cys Asp Val Gly Lys Phe Ala Lys
106          225                               230                               235                               240
107   aaa aat gaa tta gtt gaa cat tat aat atc ttc cat gat ggt aat atc   768
108   Lys Asn Glu Leu Val Glu His Tyr Asn Ile Phe His Asp Gly Asn Ile
109          245                               250                               255
110   cct gat gat tta tta aag gaa act gaa gtg aaa aaa tta gag aac cta   816
111   Pro Asp Asp Leu Leu Lys Glu Thr Glu Val Lys Lys Leu Glu Asn Leu
112          260                               265                               270
113   tta gat caa gga tcg aaa tta aat aat ttg cat gaa tta gaa aca gag   864
114   Leu Asp Gln Gly Ser Lys Leu Asn Asn Leu His Glu Leu Glu Thr Glu
115          275                               280                               285
116   aaa tta aaa gtg gaa gaa gat gaa gaa gat gaa gaa gat agt cta gat   912
117   Lys Leu Lys Val Glu Glu Asp Glu Glu Asp Glu Glu Asp Ser Leu Asp
118          290                               295                               300
119   gaa aaa aga agt gat gtt aga tca gac tca atg tca gct caa aga tca   960
120   Glu Lys Arg Ser Asp Val Arg Ser Asp Ser Met Ser Ala Gln Arg Ser
121          305                               310                               315                               320
122   ata aaa tca ttt act gct tct ttg gaa ggt tca aag agt gtt tct aaa   1008
123   Ile Lys Ser Phe Thr Ala Ser Leu Glu Gly Ser Lys Ser Val Ser Lys
124          325                               330                               335
125   ctt att ctg aat agt ggg aag aag atc aat tgt cct aag aat aat tgt   1056
126   Leu Ile Ser Asn Ser Gly Lys Lys Ile Asn Cys Pro Lys Asn Asn Cys
127          340                               345                               350
128   gat aga atg ttt tct aga gaa tat gat tta cgt cga cat ttg aaa tgg   1104
129   Asp Arg Met Phe Ser Arg Glu Tyr Asp Leu Arg Arg His Leu Lys Trp
130          355                               360                               365
131   cat gat gat aat tta caa aga att gag tca ttc tta aat agt ata gaa   1152
132   His Asp Asp Asn Leu Gln Arg Ile Glu Ser Phe Leu Asn Ser Ile Glu
133          370                               375                               380
134   aaa gaa gaa act cca gaa ggt gaa cca ttg gtt aaa aaa gcc agg atg   1200
135   Lys Glu Glu Thr Pro Glu Gly Glu Pro Leu Val Lys Lys Ala Arg Met
136          385                               390                               395                               400
137   gat tta ttg cca aat gaa aca tca gtg att tct cga taa   1239
138   Asp Leu Leu Pro Asn Glu Thr Ser Val Ile Ser Arg
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141 <210> SEQ ID NO: 3

142 <211> LENGTH: 412

143 <212> TYPE: PRT

144 <213> ORGANISM: Candida albicans

RAW SEQUENCE LISTING

DATE: 04/19/2005

PATENT APPLICATION: US/09/831,804

TIME: 16:31:51

Input Set : N:\AMC\US09831804.raw

Output Set: N:\CRF4\04192005\I831804.raw

145 <400> SEQUENCE: 3

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149      20          25          30
150 Asp Lys Ala Tyr Asn Arg Pro Ser Leu Leu Glu Gln His Leu Arg Thr
151      35          40          45
152 His Ser Asn Asp Arg Pro Tyr Lys Cys Thr Val Asp Asp Cys Asp Lys
153      50          55          60
154 Ala Phe Phe Arg Lys Ser His Leu Glu Thr His Ile Val Ser His Ser
155      65          70          75          80
156 Glu Lys Lys Pro Phe His Cys Ser Val Cys Gly Lys Gly Val Asn Ser
157      85          90          95
158 Arg Gln His Leu Lys Arg His Glu Ile Thr His Thr Lys Ser Phe Lys
159      100         105         110
160 Cys Thr Phe Glu Asn Cys Gln Glu Ala Phe Tyr Lys His Gln Ser Leu
161      115         120         125
162 Arg His His Ile Leu Ser Val His Glu Lys Thr Leu Thr Cys Lys Gln
163      130         135         140
164 Cys Asn Lys Val Phe Thr Arg Pro Ser Lys Leu Ala Gln His Lys Leu
165      145         150         155         160
166 Lys His His Gly Gly Ser Pro Ala Tyr Gln Cys Asp His Pro Gly Cys
167      165         170         175
168 Phe Lys Asn Phe Gln Thr Trp Ser Val Leu Gln Phe His Ile Lys Gln
169      180         185         190
170 Ser His Pro Lys Leu Lys Cys Pro Lys Cys Gly Lys Gly Cys Val Gly
171      195         200         205
172 Lys Lys Gly Leu Ser Ser His Met Leu Ser His Asp Asp Ser Thr Met
173      210         215         220
174 Ile Lys Ile Trp Thr Cys Asp Tyr Cys Asp Val Gly Lys Phe Ala Lys
175      225         230         235         240
176 Lys Asn Glu Leu Val Glu His Tyr Asn Ile Phe His Asp Gly Asn Ile
177      245         250         255
178 Pro Asp Asp Leu Leu Lys Glu Thr Glu Val Lys Lys Leu Glu Asn Leu
179      260         265         270
180 Leu Asp Gln Gly Ser Lys Leu Asn Asn Leu His Glu Leu Glu Thr Glu
181      275         280         285
182 Lys Leu Lys Val Glu Glu Asp Glu Glu Asp Glu Glu Asp Ser Leu Asp
183      290         295         300
184 Glu Lys Arg Ser Asp Val Arg Ser Asp Ser Met Ser Ala Gln Arg Ser
185      305         310         315         320
186 Ile Lys Ser Phe Thr Ala Ser Leu Glu Gly Ser Lys Ser Val Ser Lys
187      325         330         335
188 Leu Ile Ser Asn Ser Gly Lys Lys Ile Asn Cys Pro Lys Asn Asn Cys
189      340         345         350
190 Asp Arg Met Phe Ser Arg Glu Tyr Asp Leu Arg Arg His Leu Lys Trp
191      355         360         365
192 His Asp Asp Asn Leu Gln Arg Ile Glu Ser Phe Leu Asn Ser Ile Glu
193      370         375         380

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RAW SEQUENCE LISTING

DATE: 04/19/2005

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TIME: 16:31:51

Input Set : N:\AMC\US09831804.raw

Output Set: N:\CRF4\04192005\I831804.raw

194	Lys Glu Glu Thr Pro Glu Gly Glu Pro Leu Val Lys Lys Ala Arg Met	
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197	405 410	
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201	<212> TYPE: DNA	
202	<213> ORGANISM: Candida albicans	
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207	<211> LENGTH: 24	
208	<212> TYPE: DNA	
209	<213> ORGANISM: Candida albicans	
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215	<212> TYPE: DNA	
216	<213> ORGANISM: Candida albicans	
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221	<211> LENGTH: 25	
222	<212> TYPE: DNA	
223	<213> ORGANISM: Candida albicans	
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228	<211> LENGTH: 27	
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236	<212> TYPE: DNA	
237	<213> ORGANISM: Candida albicans	
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/831,804

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